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GenCore version 5.1.6
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June 23, 2003, 19:31:40; Search time 129 Seconds (without alignments) 5173.090 Million cell updates/sec OM nucleic - nucleic search, using sw model PCT-US02-16639-1 2176 Title: Perfect score: Sequence: Run on:

1 attgtgtctcagttggggggc......taggtgcagggttgcaaaaa 2176

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters:

441362 segs, 153338381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*
1: /cgnl\_6/ptodatcal/lina/5A\_COMB.seq:\*
2: /cgnl\_6/ptodatcal/lina/6B\_COMB.seq:\*
3: /cgnl\_6/ptodatcal/lina/6B\_COMB.seq:\*
4: /cgnl\_6/ptodatcal/lina/6B\_COMB.seq:\*
5: /cgnl\_6/ptodatcal/lina/PCTUS\_COMB.seq:\*
6: /cgnl\_6/ptodatcal/lina/PcTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		dР				
Result No.	Score	Query Match	Query Match Length DB	DB	Ð	Description
-	47.8	2.2	7218	Н	US-08-232-463-14	Sequence 14, Appl
N	37.8	1.7	548	m	US-08-828-741B-1	7
m	37.8	1.7	548	4	US-09-160-567-1	1
4	35,4	1,6	1690	~	US-08-276-452A-24	24,
Ŋ	35.4	1.6	1690	~	US-08-798-744-24	24,
9	34.8	1.6	666	4	US-09-134-001C-745	745,
7	32.8	1.5	499	4	US-09-328-111-97	97,
œ	32.6	1.5	964	m	US-08-755-587-23	23,
σ	32.6	1.5	1041	m	US-08-755-587-22	22,
10	32.6	1.5	1050	m	US-08-755-587-21	21,
11	32.6	1.5	1432	'n	PCT-US94-12912-4	4 , A
12	32.6	1.5	4770	4	US-09-000-094-45	45,
13	32.6	1.5	8010	4	US-09-521-526-2	Sequence 2, Appli
14	32.6	1.5	8010	Ŋ	PCT-US95-11859-2	'n
15	32.4	1.5	4550	4	US-09-462-136-1	Sequence 1, Appli
16	32.2	1.5	4253	m	US-08-577-483-7	7,
17	32.2	1.5	4254	~	US-08-443-639-7	7,
18	32	1.5	1031	m	US-08-828-741B-5	Sequence 5, Appli
13	32	1.5	1031	*	US-09-160-567-5	'n
20	32	1.5	1490	m	US-08-828-741B-3	'n
21	32	1.5	1490	4	US-09-160-567-3	e,
22	32	1.5	1939	4	US-08-961-527-310	310
23	31.8	1.5	4233	4	US-09-056-105-27	27,
24		1.5	84495	4	US-09-797-906-3	9
25	31.4	1.4	2277	Н	US-08-676-967-2	'n
56	31.4	1.4	2277	Н	US-08-676-974-2	Sequence 2, Appl1
27	31.4	1.4	2277	~	US-09-098-487-2	'n

Length 7218;

2.2%; Score 47.8; DB 1;

Query Match

Sequence 8, Appli Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 8, Appli Sequence 8, Appli Sequence 7, Appli Sequence 7, Appli Sequence 10, Appl Sequence 10, Appl	
US-09-323-872A-8 US-07-626-618A-12 US-08-333-977-12 US-08-977-12 US-07-928-611-8 US-07-928-611-8 US-09-06-694-8 US-09-378-014-8 US-09-378-014-8 US-09-378-074-8 US-09-178-104-8 US-09-178-104-10 US-07-928-611-10 US-07-928-611-10 US-09-10-10-10 US-09-10-10-10 US-09-178-074-10 US-09-178-074-10 US-09-178-074-10 US-09-178-074-10 US-09-178-074-10 US-09-178-074-10 US-09-178-074-10 US-09-178-074-10 US-09-178-074-10 US-09-178-074-10 US-09-178-074-10	ALIGNMENTS
<b>ゅうこうゅうこうゅうこうゅうごう</b>	
9 0 20 0 2	
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0.000000000000000000000000000000000000	

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Sequence 14, Application US/08232463
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
    APPLICANT: DORNER, F.
    APPLICANT: SCHEIFLINGER, F.
    APLICANT: SCHEIFLINGER, F.
    APLICANT: FALKNER, F. G.
    APPLICANT: FALKNER, F. G.
    APPLICANT: FALKNER, F. G.
    APPLICANT: ALGORITHM FOWLPON VIRUS
    CONTRESPONDENCE ADDRESS:
    ADDRESSEE: Foley & Lardner
    STREET: 1800 Diagonal Road, Suite 500
    CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRAT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APTICATION NOMES. 55/00/222/403
PILING DATE:
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-40G-1991
ATTORNEY/AGENT: INFORMATION:
NAME: BENT, Stephen A.
REGISTRAITON NUMBER: 29,768
REFERBNCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEFAX: (703)683-4109
TELEFAX: (703)683-4109
TELEFAX: (703)683-4109
TELEFAX: (703)683-4109
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
CLONE: PTZGFL-F1S
US-08-232-463-14
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Length 548;

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625 GCGGATTCTGCCAGCCGGGATCTGTGGGTTAACATAGACCAAATGGAAAAAGACAAAGTG 684
                                                                                                                                                                                                                                                                                                                                                     685 AAGATTCACGGGATACTTTCCAACACTCGATCGCCAAGCTGCAAGAGTGAATCTGTCCTTC 744
                                                                                                                                                                                                                                                                                                                                                                                                   97 AAAGCGAACCTGATCTTTGCAAATGGTAGCACACAAACTGCAGAATTCAAAGGTACCTTC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATITICCATITIAIGGICATITITCIAAAIGAAGICACIGIGGCAACIGGGGGITICAIA 804
                                                                                                                                                                                                                                                                                        APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                        Score 37.8; DB 3; Length 54
Pred. No. 0.068;
0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City STATE: New York CUNTRY: United States of America ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 805 TATACTGGAGAAGTTGTACAT 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 TATACTGTAGATGTTGCAGAT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Didigilo, Frank S.
REGISTRATION NUMBER: 31,346
REFRENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09160567 Patent No. 6326179 GENERAL INFORMATION:
TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                        1.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                             Query Match 1.7
Best Local Similarity 49.3
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                               ; NAME/KEY:
; LOCATION:
US-08-828-741B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 513 TCCAGAGTCCAAAGGGTTCACTGACCTGCTACTGGATGACGGACAGGACAATAACACCCA 572
                                                                    213 AGAAAAATTCGTTGGGCAGGGGAGAGATCGCGGCAGCGCCATGGCAAGGTTCCGGAG 272
                                                                                                                                                                                                                                                              333 GTTCGCCCACGGGGAGCCTGGACACCATACCAATGATTGGATTTATGAAGTTACAAAAGGC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 AAGAAATGTGGACCCTTTTAAGGCAGTAGACACAAACAGAGCCAGCATGGGCCAAGCCTC 512
                                                                                                                                                                   273 GGCCGACCTGGCCGCAGCAGGAGTTATGTTACTTTGTCACTTTTTAACAGACCGGTTCCA 332
                         Gaps
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APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CAPALITIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
CORRESPONDENCE: 14
CORRESPONDENCE ADDRESS:
Best Local Similarity 4.8%; Pred. No. 0.00024;
Matches 19; Conservative 214; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1089 RRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCG 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             573 GATAGAGGACACGGATCACAATTACTACATTTCTCG 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Didigilo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08828741B Patent No. 6043069
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TELEFAX: (516) 742-4366
TELEEX: 230 901 SANS UR
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 548 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11530
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               625 GCGGATTCTGCCAGCCGGGATCTGTGGGTTAACATAGACCAAATGGAAAAAGACAAAGTG 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                685 AAGATTCACGGGATACTTTCCAACACTCCATCGGCAAGCTGCAAGATGAATCTGTCCTTC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                745 GATTTICCATTTTATGGICATTTTCTAAATGAAGTCACTGTGGCAACTGGGGGTTTCATA 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chen, Chao-Guang
APPLICANT: Mau, Shalo-Lim
APPLICANT: Du, He
APPLICANT: Du, He
APPLICANT: Gane, Alison M
APPLICANT: Gane, Alison M
APPLICANT: Clarke, Adrienne E
TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes
NUMBER OF SEGUENCE: 9
ADDRESSEDE: Greenlee and Winner, P.C.
ADDRESSEDE: Greenlee and Winner, P.C.
ADDRESSEDE: ACCOUNTION OF THE ARABINOGALACTAIN OF THE ACCOUNTY OF 
                                                                                                                                                                                                                                    1.7%; Score 37.8; DB 4; Length 548;
49.3%; Pred. No. 0.068;
tive 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/276,452A
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATORNEY/AGENT INFORMATION:
NAME: CARITHER, Jennie M.
REGISTRATION NUMBER: 34,464
REBERENGE/POCKET NUMBER: 27-91A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8089
TELERAX: (303)499-8089
TELERAX: (303)499-8089
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1590 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colorado
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-276-452A-24/c
; Sequence 24, Application US/08276452A
; Patent No. 5646029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           805 TATACTGGAGAGGTTGTACAT 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                      Query Match
Best Local Similarity 49.32
Thes 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                  CDS
1..548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80303
                                                                         NAME/KEY:
COCATION:
US-09-160-567-1
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1581 TGACAGTGCAGCTGAGAAGAAGGAGGAACCCTCCATGCAGGCCTCATTGTTGGAATTCT 1640
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LOCATION: 135..179
OTHER INFORMATION: /note= "Derived amino acid sequence
OTHER INFORMATION: corresponding to the peptide sequence by protein
OTHER INFORMATION: microsequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 135..179
OCHER INFORMATION: Ala; 37 and 39 can also be undetermined residues'
                                                                      LOCATION: 1..38

OTHER INFORMATION: /note= "Nucleotide sequence orners information: obtained by PCR which does not overlap with the OTHER INFORMATION: obtained by PCR which does not overlap with the OTHER INFORMATION: cDNA clone" PEATURE:

NAME/KEX: misc_feature
LOCATION: 60..128

OTHER INFORMATION: segment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: 135..1.79
OTHER INFORMATION: /note= "Amino acids 27 to 36, 38,
OTHER INFORMATION: and 40 are identical to that in the peptide
OTHER INFORMATION: obtained by direct microsequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/08798744

Patent No. 5830747

GENERAL INFORMATION:
APPLICANT: Chen, Chao-Guang
APPLICANT: Mau, Shaio-Lim
APPLICANT: Man, Alison M
APPLICANT: Gane, Alison M
APPLICANT: Clarke, Adrienne E
TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.6%; Score 35.4; DB 1; Length 1690;
Best Local Similarity 61.3%; Pred. No. 0.82;
Matches 57; Conservative 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISN PC compatible
COMMUTER: ISN PC compatible
COMPUTER: ISN PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,744
FILING DATE: 13-FEB-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1641 CATCTTGGTCCTCATTATAGCAGCGGCCATTCT 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1230 CATTCTTGATATCATAATAATACTTGCCATTTT 1198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abba.
STREET: 53/0...
CITY: Boulder
STATE: Colorado
...mov: United States of America
                                                  misc_feature
60..1442
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US-08-798-744-24/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-276-452A-24
                                                     NAME/KEY:
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1347 GGACTGGGTGGACAGTGGATGCCCGGAAGAGGTACAGTCAAAAGAGAAGATGTGTGAGAA 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 770 TAAATGAAGTCACTGTGGCAACTGGGGGTTTCATATATACTGGAGAAGTTGTACATCGAA 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      830 TGCICACAGCTACACAGTATATAGCTCCTTTAATGGCAAATTTTGATCCCAGTGTATCCA 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 ACAATGGGTCTGGCGCTGAGATTGGACATTTAAGAGCTGATTTTGATCAACGTTTTCAAT 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 GGACTGTGGCCAGAGTTGGGACCCTGGAGCATCTTGTCTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.6%; Score 34.8; DB 4; Length 993; Best Local Similarity 54.8%; Pred. No. 0.9; Matches 69; Conservative 0; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.5%; Score 32.8; DB 4; Length 499;
59.8%; Pred. No. 2.5;
.ive 0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lewis, Marcia E.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILLE REPRENSE: CCD-27 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FASTER FOR NOS: 850
SOFTWARE: FASTER FOR WINDOWS VERSION 3.0
                                                CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                    CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NOS: 5674
LENGTH: 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 97, Application US/09328111
Patent No. 626333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Rathleen E.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll Anna APPLICANT: Carroll Steven E.
APPLICANT: Carroll Anna APPLICANT: Ford, Donna M.
                                                                                                                                                                                                                                                                                 ; TYPE: DNA; CRANISM: Staphylococcus epidermidis
US-09-134-001C-745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KET: misc_feature

: LCCATION: (1)...(499)

: OTHER INFORMATION: n = A,T,C or G

US-09-328-111-97
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Best Local Similarity 59.8
Matches 55; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    890 GAAATT 895
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Sequence 745, Application US/09134001C

Patent No. 6380370

Patent No. 6380370

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE. OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1581 TGACAGTGCAGCTGAGAAGAAGGAGGAACCCTCCATGCAGGCCTCATTGTTGGAATTCT 1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "Derived amino acid sequence corresponding to the peptide sequence by protein microsequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 135.7179 COTHER INFORMATION: /note= "Amino acid 26 may also be OTHER INFORMATION: Ala; 37 and 39 can also be undetermined residues' US-08-798-744-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1..38
UNCHEN INFORMATION: /note= "Nucleotide sequence
OTHER INFORMATION: obtained by PCR which does not overlap with the
OTHER INFORMATION: cDNA clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 135.179
OTHER INFORMATION: /note= "Amino acids 27 to 36, 38,
OTHER INFORMATION: and 40 are identical to that in the peptide OTHER INFORMATION: obtained by direct microsequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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1.6%; Score 35.4; DB 2; Length 1690;
Best Local Similarity 61.3%; Pred. No. 0.82;
Matches 57; Conservative 0; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 60.128
LOTER INFORMATION: /note= "Predicted transmembrane
OTHER INFORMATION: segment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1641 CATCTTGGTCCTCATTATAGCAGCGGCCATTCT 1673
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/276,452
FILING DATE: 18-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carturhers, Jenile M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 27-91A
TELEPHONE: (303,499-8089)
TELEPAX: (303,499-8089)
TELEPAX: (303,499-8089)
TELEPAX: (49617824
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHRACTERISTICS:
LENGTH: 1690 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: CDNA
FRANDRE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 135..179
OTHER INFORMATION: /note
OTHER INFORMATION: correc
OTHER INFORMATION: micro
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LOCATION: 60..1442
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225 CCCCTTTTTTACCCCCAGTGGTATGTGGGAGTTTGTTTCATACACCAAAGTTTGTAAG 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706 AACACICATCGGCAAGCIGCAAGAGIGAAICTGICCTTCGAITTTCCAITTTAIGGICAI 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Futreal, Phillip A
APPLICANT: Wooster, Richard F
APPLICANT: Wooster, Alan
APPLICANT: Stratton, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: Jentification and sequencing of the BRCA2 cancer
TITLE OF INVENTION: ausceptibility gene and uses thereof.
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CIIY: Raleigh
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.5%; Score 32.6; DB 3; Length 964; Best Local Similarity 46.0%; Pred. No. 4.4; Matches 110; Conservative 0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-LUGYMS-LOUS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 952555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGNEY INFORMATION:
NAME: Kenneth D 51bley
REGISTRATION NUMBER: 34.65
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 964 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
                 1407 GACAGAGCCAGGAGAGACATCTCAAACTACCA 1438
                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                       Sequence 23, Application US/08755587 Patent No. 6045997 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
501..615
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-755-587-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ğ
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Sequence 22, Application US/0875587

Patent No. 604597

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Futreal, Phillip A

APPLICANT: Ashworth, Alan

APPLICANT: Ashworth, Alan

TITLE OF INVENTION: Materials and methods relating to the

TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer

TITLE OF INVENTION: susceptibility gene and uses thereof.

NUMBER OF SEQUENCES: 222

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bell Seltser Park & Gibson

STREET: 310 UGB Plaza, 3605 Glenwood Avenue, PO Drawer 31107

CITY: Ralein

STATE: NCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 646 CIGIGGGITAACAIAGACCAAAIGGAAAAAGACAAAGIGAAGAIICACGGGAIACIIICC 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                706 AACACTCATCGGCAAGCTGCAAGAGTGAATCTGTCCTTCGATTTTCCATTTAATGGTCAT 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.5%; Score 32.6; DB 3; Length 1041;
Best Local Similarity 46.0%; Pred. No. 4.7;
Matches 110; Conservative 0; Mismatches 129; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: NC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: BEACHINE: PC-DOS/MS-DOS
SOFTWARE: PATCHIN RCLEASE #1.0, Version #1.25 (EPO)
SOFTWARE: PATCHIN RCLEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 23-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 952355.0
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Renach D SIDLEY
RESIGNATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
SEQUENCE TOWNER: 31,665
SEQUENCE TOWNER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
FEVENCE CHARACTERISTICS:
SEQUENCE TOWNER: 31,665
REPERENCE/DOCKET NUMBER: 5405-135
FEVENCE TOWNER: 5405-135
FEVENCE TOWNER: 5405-135
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MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1041 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
501..541
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LOCATION:
FEATURE:
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RESULT 9
US-08-755-587-22
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US-08-755-587-22
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766 ITTCTAAATGAAGTCACTGTGGCAACTGGGGGTTTCATATATACTGGAGAAGTTGTACAT 825

623 CCCCTITITITACCCCCAGIGGIAIGTGGGAGITIGTICATACACCAAAGTITGTGAAG 682

826 CGAAIGCICACACCACACCACACATAIAGCICCITIAAIGGCAAAITITGAICCCAGIGI 884 

766 TITCIAAATGAAGTCACTGTGGCAACTGGGGGTTTCATATATACTGGAGAAGTTGTACAT 825

706 AACACTCATCGGCAAGCTGCAAGAGTGAATCTGTCCTTCGATTTTCCATTTTATGGTCAT 765

503 CTGTTGTTCTACAATGTACACATGTAACACCACAAAAGAGATAAGTCAGGTATGATTAAAA 562

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pct-us02-16639-1.rni
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40 40 40 40 40 40 40 40 40 40 40 40 40 4	RESULT PCT-USS > Seque   GENE   FI		5 a	T NIC	PCT-US Ouer Best Matc	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	5 G
AATCCTITITATTCTTAGAATGCTAGAAATGTTAATAAAATAA	usy 08755587  hillip A  tichard F  Alan  Atchael R  aterials and methods relating to the  dentification and sequencing of the BRCA2 cancer  acceptability gene and uses thereof.	NCE ADDRESS: 1 Bell Seltzer Park & Gibson 1 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107 1eigh C C AAABLE FORM: PPE: Floppy disk	ompatible PC-DOS/MS-DOS Release #1.0, Version #1.25 (EPO) ATA: US/08/755,587 A. 1996	GB 9523959.6 1995 GB 9525555.0 1995 GB 9617961.9 1100N:	NAME: Kennerh D Sidley  REGISTRATION NUMBER: 31,665  REFERENCE/DOCKET NUMBER: 5405-135  REFERENCE/DOCKET NUMBER: 5405-135  REPRENCE/DOCKET NUMBER: 5405-135  SEQUENCE CHARACTERISTICS: FOR THE POTT-US  LENTH: 1050 base pairs  TYPE: nucleic acid  STRANDEDNESS: double  STRANDEDNESS: double  MALECULE TYPE: DNA (genomic)	DS 02550 xon 01550	atch 1.5%; Score 32.6; DB 3; Length 1050; cal Similarity 46.0%; Pred. No. 4.7; 110; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
Db Oy Oy Db Db	NESOLI OS-08-17 Seque Seque GENE APP APP APP APP APP APP APP APP APP AP	8		A B E	OTNI SE SE	FI FI FI COS-08-7	Query M Best Lo Matches

646 CTGTGGGTTAACATAGACCAAATGGAAAAGACAAAGTGAAGATTCACGGGATACTTTCC 705

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1252 GGTTGTGCCCTTGTGTGTCTCGCAGATTGGTTTCAACTGCAGTTGGTGCAGCAAACTT 1311
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                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEBM FC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12912
FILING DATE:
CLASSIFICATION:
NAME: Spitals. John P.
REGISTRATION:
REGISTRATION NUMBER: 1920-341
FREFERENCE/DOCKET NUMBER: 1920-341
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 1937-11001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 1937-11001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SULT 11

--US94-12912-4/C
Sequence 4, Application PC/TUS9412912
Sequence 4, Application PC/TUS9412912
Sequence 6, Application PC/TUS9412912
GENERAL INFORMATION:
GENERAL INFORMATION:
COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TANNSDUCTION OF CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCES: C/O Robbins, Berliner & Carson
STREET: 201 North Figueroa Street, Fifth Floor
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA
594-12912-4
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760 GCTGTGAATCGGTGCTGGCAACTGGAGAGAGAGAGCCAGATCCTGGAGAGGCAACCCA 702

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405 TGAAGAGGGGGTAGAAGTGGACTCTCAAGCATACAACCACGAGGAAAAGAAATGTGGA 464
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                                                                                     ...in

C.A. John Cooper
FRAZER, Ian
FRAZER, Ian
FRAZER, Ian
MULLIAMS, Mark Philip
MOLONEY, Margaret Bridget
MOLONEY, Margaret Bridget
HOLLAMS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
RADRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY. ..
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COUNTRY: U.S.A.

ZIP: 20007-2007

ZIP: 20007-5109

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: FLOPPY disk

SOFTWARE: Patentin Release #1.0, Version #1.30

CURENT APPLICATION NOMBER: US/09/000,094

FILING DATE: 21-Apr-1996

APPLICATION NOMBER: WO PCT/AU36/00473

FILING DATE: 27-JUL-1995

ATTORICATION NOMBER: AD PN 4439/95

ATTORICATION NOMBER: 29.768

REFERENCE/DOCKET NUMBER: 29.768

TELEPHONE: (202) 672-5399

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 4770 base pairs

STRANDEDNESS: SINGLE

TYPE: nucleic acid

TYPE: nucleic acid

TOTAL TELEFATOR TOTAL TOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Indels
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RESULT 12
US-09-000-094-45
; SGOONCE 45, Application US/09000094
; Partent No. 6365160
; GENERAL INFORMATION:
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1252 TGAAGTGGAAGCTGGAACGGAACGCTAGAGAAACATGGCGTCCCGGAAAATGGGGG 1311
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RESULT 13

US-09-221-526-2

Sequence 2, Application US/09521526

Patent No. 629965

GENERAL INFORMATION:

APPLICANT: JANSEN, KATHRIN U.

APPLICANT: HOFMANN, KATHRIN U.

APPLICANT: HOFMANN: 6A

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

APPRICANT: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER: RAHMAN PCONGALIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACALLE FORM:

MEDIUM TYPE: FORDAY

COMPUTER: BACALLE FORM:

MEDIUM TYPE: FORDAY

COMPUTER: BACALLE FORM:

MEDIUM TYPE: FORDAY

COMPUTER: BACALLE FORM:

MEDIUM TYPE: FORDAY

COMPUTER: BACALLIN Release #1.0, version #1.25

CURSENT APPLICATION DATA:

PRIOR APPLICATION DATA:

REPLICATION NUMBER: US/09/521,526

FILING DATE: 22-SEP-199

TELECOMMUNICATION NUMBER: 19307

TELECOMMUNICATION NUMBER: 136,099

REFERENCE/DOCKEN NUMBER: 136,099

REPERPONE: (908) 594-6734

TELECOMMUNICATION NUMBER: 136,099

REPREPROME CHARACTERISTICS:

LENGTH TOLLAL CACID

TELECOMMUNICATION NUMBER: 136,099

REPREPROME CHARACTERISTICS:

LENGTH TOLLAL CACID

TELECOMMUNICATION NUMBER: 136,099

REPREPROMENCE CHARACTERISTICS:

LENGTH TOLLAL CACID

TELECOMMUNICATION NUMBER: 136,099

REPREPROMENCE CHARACTERISTICS:

LENGTH TOLLAL CACID

TELECOMMUNICATION NUMBER: 136,099
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1.5%; Score 32.6; DB 4; Length 8010;
Best Local Similarity 51.0%; Pred. No. 18;
Matches 77; Conservative 0; Mismatches 74; Indels 0.
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GENERAL INFORMATION:
APPLICANT: JANSEN, KATHRIN U.
APPLICANT: HOFMANN, KATHRIN J.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLLOMA VIRUS TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1372 AGGCCCACAACAGTGTACGGGAGCATGCA 1402
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PCT-US95-11859-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 TGAAGAGGGGGTAGAAGTGGACTCTCAAGCATACAACCACAGGTGGAAAAGAAATGTGGA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 CCCTTTTAAGGCAGTAGACACAAAACAGAGCCAGCATGGGCCAAGCCTCTCCAGAGTCCAA 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Carstea, et al.
TILLE OF INVENTION: Genes for Niemann-Pick Type C Disease FILE REFERENCE: 429-5399.
FULE REFERENCE: 4239-5399.
CURRENT APPLICATION NUMBER: US/09/462,136
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/US98/13862
PRIOR APPLICATION NUMBER: US 60/051,682
PRIOR FILING DATE: 1997-07-03
                                                                                                                                                                                  MEDIUM III.

COMPUTER: IBM PC_Compatible
COMPUTER: IBM PC_COMPAGE.

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11859
FILING DATE:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,468
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: CARTY CHRESTINE E.
RETERRATION NUMBER: 19307 PCT
FELECOMMUNICATION INFORMATION:
TELEPONE: (908) 594-4720
INFORMATION RE: (908) 594-4720
INFORMATION PO: 2:
SEQUENCE GHARACTERISTICS:
LENGTH: 8010 base pairs
                                                    - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1372 AGCGCCCACAACAGTGTACGGGAGCATGCA 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.5%; Score 32.6; DB Best Local Similarity 51.0%; Pred. No. 18; Matches 77; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525 AGGGTTCACTGACCTGCTACTGGATGACGGA 555
CORRESPONDENCE ADDRESS:
ADDRESSE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE -
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09462136 Patent No. 6426198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Ver. 2.0
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SOFTWARE: Patentin Ve
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: 11:
; MOLECULE TYPE:
PCT-US95-11859-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-462-136-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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June 23, 2003, 17:38:49 ; Search time 486 Seconds (without alignments) 10083.021 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                           1 attgtgtctcagttgggggc......taggtgcagggttgcaaaaa 2176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqr-embl/NA1998.DAT:*
/SIDS2/gcgdata/geneseq/geneseqr-embl/NA1999.DAT:*
/SIDS2/gcgdata/geneseq/geneseqr-embl/NA2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqr-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqqr-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqr-embl/NA2001B.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4370478
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                          2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
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			Description	Mouse Tumour Endot	Mouse Tumour Endot	Human polynucleoti	Human DNA encoding	Stem cell growth f	Human Tumour Endot	Human Tumour Endot	Nucleotide sequenc	Stem cell growth f
SUMMARIES			ID		ABL92137	AAI58224	AAS46160	AAH23066	ABL92080	ABL92088	AAC87054	AAH23067
			DB :	24	24	22	22	22	54	24	22	22
			re Match Length DB 1	2009	2010	2817	2594	3095	2157	2159	2557	1590
	dР	Query	Match	89.0	89.0	6.79	67.9	66.2	65.4	65.4	65.4	56.9
			Score	1935.6	1935.6	1478.2	1476.6	1440.4	1423.8	1423.8	1423.4	1238
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St Croix B, Kinzler KW, Vogelstein B;

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O	10	1195.2	_:	2668	22	AA160009	Human polynucleoti
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	12	1195.2	_	2668	22	AAH75398	polynucleot
	13	1195.2	_	2668	22	AAH23063	Stem cell growth f
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	15	1165.2	53.5	2275	22	AA158223	polynucleot
	16	1031.6	۲.	1351	22	AAH23068	Stem cell growth f
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	19	727.8	Ψ.	1101	21	AAC74708	Human ORFX ORF263
	20	393.6	÷.	2320	24	ABL92103	Human Tumour Endot
	21	393.6	'n.	4640	24	ABL92077	Human Tumour Endot
	22	384.4	۲.	464	22	AAH23054	Stem cell growth f
	23	365.6	'n	2833	24	ABL92083	Mouse Tumour Endot
	24	365.6	'n	2840	24	ABL92136	Mouse Tumour Endot
	25	347.6	'n	1201	21	AAC77340	Human ORFX ORF2895
O	56	343.6	'n	406	22	AAH23062	Stem cell growth f
	27	333	'n.	820	22	AAH93283	Human tumour endot
	28	333	'n.	820	22	AAH93285	Human tumour endot
O	53	328.6	'n.	392	22	AAH23051	Stem cell growth f
	30	328.4	'n	412	22	AAH23058	cell growth
	31	322.4	٠.	498	55	AAH23048	Stem cell growth f
	32	321.8	÷	1141	22	AAK61650	Human immune/haema
	33	318.6	÷	479	22	AAH05765	CDN
	34	298	e,	366	22	AAH23042	cell growth
O	32	295	æ.	382	22	AAH23061	cell growth
O	36	290	w.	417	22	AAH23052	cell growth
O	37	275.2	ä	416	22	AAH23060	tem cell growth
	38	269.3	ď	430	55	AAH23056	cell g
	39	266.6	ď	348	22	AAL22512	breast canc
	40	366	ď	334	22	AAH23043	cell g
	41	265.6	ď	347	22	AAL13643	it cand
	42	260.6	ď	415	22	AAH23053	Stem cell growth f
	43	231.4	ö	534	55	AAH93287	Human tumour endot
	44	229.8	ö	323	24	ABN17873	O.R.
	45	217.8	ö	422	22	AAH23044	Stem cell growth f
						ALIGNMENTS	
RE:	RESULT 1	디호					

Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker: pan-endothelial marker; immunostimulant; antianglogenic; tumour; neoanglogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatold arthritis; psoriasis; gene; ss. Mouse Tumour Endothelial Marker polynucleotide SEQ ID NO 185. ABL92084 standard; cDNA; 2009 BP. 02-AUG-2000; 2000US-222599P. 11-AUG-2000; 2000US-224360P. 11-APR-2001; 2001US-282850P. 01-AUG-2001; 2001WO-US24031 (first entry) WO200210217-A2. Mus musculus 30-MAY-2002 07-FEB-2002. ABL92084; 

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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (ERM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antianglogenic activity. They are useful for inhibiting tumour, polycystic kidney disease, subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and sositasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed as are marker coligonucleotide sequences: tumour endothelial markers (FEM) ABL9996-ABL92041 and ABL9143-ABL92191; normal endothelial markers (FEM) ABL9996-ABL92042-ABL92042, and pan-endothelial markers (FEM) ABL91995.
                                                     An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth -
                                                                                                                                                                  Disclosure; Page 133-134; 331pp; English
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Sequence 2009 BP; 624 A; 461 C; 475 G; 449 T; 0 other;

ö GTTATGTTACTTTGTCACTTTTTAACAGACCGGTTCCAGTTCGCCCACGGGGAGCCTGGA 354 414 534 714 774 600 294 CACCATACCAATGATTGATTATGAAGTTACAAACGCTTTTCCTTGGAATGAAGAGGGG 180 474 594 360 654 420 480 834 894 TCAACTGTCAGATATTTTGATAATGGCACAGCTCTTGTTGTCCAGTGGGACCATGTCCAC 954 9 GAGAGGTCGCGGCAGCGGCATGGCAAGGTTCCGGAGGGCCGACCTGGCCGCAGCAGGA CGGCAAGCTGCAAGAGTGAATCTGTCCTTCGATTTTCCATTTTATGGTCATTTTCTAAAT CGGCAAGCTGCAAGAGAGAATCTGTCCTTCGATTTTTCCATTTTATGGTCATTTTCTAAAT GAGAGAGGTCGCGCCAGCGCATGGCAAGGTTCCGGAGGGCCCGACCTGGCCGCAGCAGCA CACCATACCAATGATTGGATTTATGAAGTTACAAACGCTTTTCCTTGGAATGAAGAGGGG GTAGAAGTGGACTCTCAAGCATACAACCACAGGTGGAAAAGAAATGTGGACCCTTTTAAG GCAGTAGACACAAACAGAGCCAGCATGGGCCAAGCCTCTCCAGAGTCCAAAGGGTTCACT GACCTGCTACTGGATGACGGACAGGACAATAACACCCGAGATAGAGGAGGACACGGATCAC 595 AATTACTACATTTCTCGGATATATGGTCCAGCGGATTCTGCCAGCCGGGATCTGTGGGTT **AACATAGACCAAATGGAAAAAGACAAAGTGAAGATTCACGGGATACTTTCCAACACTCAT** GAAGTCACTGTGGCAACTGGGGGTTTCATATATACTGGAGAAGTTGTACATCGAATGCTC 835 ACAGCTACACAGTATATAGCTCCTTTAATGGCAAATTTTGATCCCAGTGTATCCAGAAAT Gaps ö h Similarity 99.8%; Pred. No. 0; 4; Indels 0; Mismatches Matches 1938; Conservative Query Match Best Local S 241 361 481 235 295 61 121 **4**15 181 475 535 301 655 715 355 9 PP ద g Q ò g ò g Óλ g ö 셤 δ g ò g ò ò ò ద

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                                                                                                                                                                                                                                                                                                                                                                                                             Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antianglogenic; tumour; neoanglogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis; gene; ss.
                              TTCACAAGGAACATCTCCGGTGGACTTGCCAGGAGTGTGACGAGATGACGATGCTTTTGG
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

26-DEC-2000; 2000WO-US34263

WO200153312-A1.

26-JUL-2001

leukaemia; ss Homo sapiens.

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                                                                   AGATGCTCCAGTGGATTTGATCGCCATCGGCAGGACTGGGTGGACGAGTGGATGCCCGGAA 1374
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTAGCGAAACTGTCAGAGGCCTCCGGATCCCAACCCCAAGACTCACCAGCAGCTCGGCC 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TIGIGICICAGIIGGGGGCIGCGAGGGIGACAAGIIGCAGIGAGAGCICCCGAAGIICGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
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Yang Y,
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25-APR-2000; 2000US-0552317.
9-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
19-OCT-2000; 2000US-0653450.
29-NOV-2000; 2000US-0727344.
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Best Local Similarity 82.7
Matches 1815; Conservative
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P-PSDB; AAM39068.
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Wang Z, W
Zhou P,
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Human polynucleotide SEQ ID NO

(first entry)

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AAI58224;

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ID AAI:
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AAI58224 standard; cDNA; 2817

RESULT

1822 1368 1882 1425 1425 1936 1936 1545 2016 11725 2116 1725 2176 1725 2176 1725 2236 1904 2416 1964 2467	2526 2079 2586 2646
AACTGGGGTGGCTGGTAAAAACTGGGGGGGGGGGGGGGG	CCCAGGRARGI NA NA N
	CTGCTGTAGCCTGAA-GAAGACTTCTGGACAAGCTCAGCCCAGGAAACAAGGGT GAAAGGAAAACTTATACAAGACTCTGTACAATGATTAAAAAAAA
	2468 CTGCTGTAGCCTGAA-GAAGACAAGATTCTGGACAAGCT 2020 GAAAGGAAACTCAGACTTGTACAAGATACAAAT 2527 AAACAAAACTTAAAACTTATACAAGATACCATTTACACT 2080 GAATGACATCCATGGTTCACAAGGAACATCTCCGGTGGAC 2180 GAATGACATCCATGTTCACAAGGAACATCTCCGGTGGAC 2140 TGACGATCTTTAGTTTAGGTTCACGAACATCTCCGTGGAC 2140 TGACGATCTTTGGTTTAGGTCAGGGTTGCAAA 217 2647 TTATAATGCTTTTGGCTTAGGTGCAGGGTTGCAAA 2681 160 AAS46160; AAS46160; Human DNA encoding PRO polypeptide sequence #236
AACAGATGTGGCCCTGTGTATCTCTCAGATI AACAGATGTGGCCCTGTGTATCTTCTCAGATI CTTCAAAGATGTCCAGTGGATTTGATCGCAT CTTCAAAGATGTTCCAGTGGATTTGATCGCAT CTTCAAAGATGTTCCAGTGGATTTGATCGTCA CCGGAAGAGTACTCCAGTGGATTTGATCGTCA CCTGAAGATGTTCCAGTGAAAGAAGATGTGT CTTCAAACTACCACGACCTCCCACAGAGAAGATGTGT CTTCAAACTACCACGACCTCCCACAGAGAAGATGTGT CTTCAAACTACCACACACACACACACAGAAGAAGATGTGT AGAAGAGAGTGAACTTCTCAGATTCCACAGAGAATGTTTTTTTT	-GAAGACAAG ACTTGTACAA ACTTATACAA ACTTATACAA TTCACAAGG TTTACCAGGG TTTAGGTGC T
	TGTAGCCTGAA-G GGAAAACTCAGAC
1763 AACAGA 1309 CTTCAA 1369 CTTCAA 1369 CCGGAA 1426               1426             1937 CTCGAA 1937 CTCGAA 1937 CTCGAA 1957 AGAAGA 1546 GCCCTA 1546 GCCCTA 1546 GCCCTA 1546 GCCCTA 1546 GCCCTA 1546 GCCCTA 1546 GCCCTA 1546 GCCCTA 1546 GCCCTA 1546 GCCCTA 1656 GCCCTT 1756 GCCCTT 1756 GCCCTT 1756 GCCCTT 1756 GCCTTA 1756 GCCTTA 1757 GCCTTA 1757 GCCTTA 1757 GCCTTA 1757 GCCTTA 1757 GCCTTA 1757 GCCTTA 1757 GCCTTA 1757 GCCTTA	2468 CIGCTGTAGG 2020 GAAAGGAAAA 2527 AAACAAAAAA 2080 GAATGACATG 2180 TAGGATGCATG 2140 TGACGATGCATG 2140 TGACGATGC 2140 TGACGATGC 2147 TTATAATGC AAS46160 standard; AAS46160; Human DNA encoding
	Db         2468           QY         2020           Db         2527           QY         2080           Db         2587           QY         2140           Db         2647           RESULT 4         AAS46160           XX         AAS46160           XX         AAS46160           XX         AX46160           XX         AX46160           XX         AX46160           XX         XX           DT         18-DEC-2           XX         XX           DT         Human DM
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	AGAAATTCCCAATCTCCAGATATTTGATAATGCCACCACTGTGGCCCACGGGGCCCATGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT
COAGGGTCTC	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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CCAGGGATAA	
GCCCCATCCC GCGCCTATTC GGGGGGGGG	ACCCAACTGT ATCTCAGGA ACCTGCAGGA ACCTCCAGGAATCAT ACACCCAGT ACCCAGT ACACCCAGT ACACCCAGT ACACCCAGT ACACCCAGT ACACCCAGT ATCACCAATGT ATCACCAATGT AAATTACCAA AAATTACCAA GTGTGGCCCATGT AAATTACCAA
	GGAN,
169 691 229 229 289 803 349 863 923 469 923 1103 1103 769 1223 1223 1223 1343	

pct-us02-16639-1.rng

PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss; dog; eat; pig; goat; rabbit; tumour necrosis factor alpha; TMF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder; PCR primer

Homo sapiens,

WO200168848-A2

20-SEP-2001

28-FEB-2001;

2000WO-USO5841.
2000WS-USO5841.
2000WS-USO5841.
2000WS-USO5841.
2000WS-USO588.
2000WS-USO588.
2000WS-USO588.
2000WS-USO588.
2000WS-USO588.
2000WS-USO58.
200 01-MAR-2000; 02-MAR-2000; 06-MAR-2000; 14-MAR-2000; 114-MAR-2000; 15-MAR-2000; 21-MAR-2000; 21-MAR-2000; 21-MAR-2000; 22-MAR-2000; 29-MAR-2000; 29-MAR-2000; 11-APR-2000; 11-A

30-MAY-2000; 2000MO-US11941. 02-UNA-2000; 2000MO-US15264. 05-UNA-2000; 2000MO-US15264. 28-UDL-2000; 2000MO-US20710. 22-AUG-2000; 2000MO-US23328. 24-AUG-2000; 2000MO-US23328. 08-NOY-2000; 2000MO-US23678. 01-DEC-2000; 2000MO-US32678.

(GETH ) GENENTECH INC

Goddard A, Godowski PJ, Gurney AL; Wood WI, Zhang Z; Chen J, Desnoyers L, 1th V, Watanabe CK, W Smith V, Baker KP, an J,

WPI; 2001-602746/68. P-PSDB; AAU29259.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals to screen for modulators of the compounds -

Claim 2; Fig 471; 774pp; English.

Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample

of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal: Mammals include dogs, cats.cattle, horses, sheep, pigs, goets and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours; in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.

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Sequence 2594 BP; 721 A; 645 C; 639 G; 589 T; 0 other;

Query Match 67.9%; Score 1476.6; DB 22; Length 2594; Best Local Similarity 82.6%; Pred. No. 0; Maxches 1814; Conservative 0; Mismatches 334; Indels 47; (

2 TTGTGTCTCAGTTGGGGGCTGCGAGGGTGACAAGTTGCAGTGAGAGCTCCCGAAGTTCGG AGAGGGTTCAGCT------GTCTCCTTCACTTCTGTTACCCGGAGTGAAAT 62

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558 440 AGAGGGCTGCGCTCCTACTCGCGTTCGTTCTTCTTCTCGGTTCCCTACTGTGAAT CCTAGCGAAACTGTCAGAGGCCTCCGGATCCCCACCCAAGACTCACCAGCAGAGCTCGGCC 109

GTGTCGCCCCATCCCCAGGGATAACCCCGGAGCCCAGGGTCTCAAGAAAAATTCGTTGG CGGTCGTGCCTATTGCATCGGGAGCCCCCGAGCACCG------GCGAAGGACTGGCGG 169 559

GCAGGGGAGAGAGAGCGCGCGCAGCGGCATGGCAAGGTTCCGGAGGGCCGACCTGGCCGCA 288 229

GCAGGAGTTATGTTACTTTGTCACTTTTTAACAGACCGGTTCCAGTTCGCCCACGGGGAG 671 289

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468 791 409

910 CICAAGGCGTAGACACGAACCAAGCGAGCAAGCCTCCTCCTGAGCCCCAGAAGC TITAAGGCAGTAGACACAAAAGAGCCAGCATGGGCCAAGCCTCTCCAGAGTCCAAAGGG 469

TTCACTGACCTGCTACTGGATGACGGACAGGACAATAACACCCAGATAGAGGAGGACACG 529 911

648 GATCACAATTACTACATTTCTCGGATATATGGTCCAGCGGATTCTGCCAGCCGGGATCTG 971 GACCACAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTTA 583

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209 1091 CTAAATGAAGTCACTGTGGCAACTGGGGGTTTCATATACTGGAGAAGTTGTACATGGA 169

Oy 1905 GCTTATGCA Db 2285 GCTTATACC OY 1965 CTGCTGTAG OY 1965 CTGCTGTAG OY 2020 GAAAGGAAA OY 2020 GAAAGGAAA OY 2039 AAACAAAAA OY 2039 GAATGACAT OY 2080 GAATGACAT OY 2080 GAATGACAT OY 2080 GAATGACAT OY 2080 GAATGACAT OY 2050 GAAT	YULT 5 123066 AAH23066 standar AAH23066; 17-SEP-2001 (fil Stem cell growth Stem cell growth degenerative dist generative dist Gytostatic; noot generative stem Key	ET CDS XX XX WO200153500-A1. XX PX WO200153500-A1. XX PX 23-DEC-2000; 20000 PR 21-JAN-2000; 20000 PR 07-APR-2000; 20000 XX PX L1-APR-2000; 20000 XX PX	XX DR WPI; 2001-451909/4 DR P-PSDB; AAB86394. XX PT Isolated polypepti PT treatment of leuke PT Alzheimer's diseas XX CS The invention proving The proving The proving CS The properties and CS Stem cell growth is CS stem cell growth in CS stem cell growth is CS stem cell growth is CS stem cell grow
CTACGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAGTCGTACATCGAAATCACTGGAAATCACTGGGAAGTCGTACATCGAAATTTGATCCCAGTGTACATCGAAGTTAATGGCAAATTTTGATCCCAGTGTATTCCATGTAACACGCCACACGAAATTTTGATCCAGTGTATTCCAGTGCAAATTTTGATAATGGCAAATTTTGATTACACTGTCAGTGGGAACTTTCGATCCAGTGGGACCATTGATTCAACTGTCAGTGGAACATTTTGATAATGGCACAGTCTTGTTGTCCAGTGGGACCATTGATACAACTGTCAGTGGGACCATTGATCAACTGCAGTGGGAACATTCAACTGTCAGTGGGACCATTGATACAACTGTCAGTGGGAACCATTCAGTCCAGTGGGACCATTGATACAACTTCAGTGGGCACCTCTCATGGTTCAACTGTCAGTGGGAACATTCAACTGTCAGTGGGAACCATTCAGTGGCACCATTGATCAATTTTTTTT	ACCAATCAGTGAAAGTGGGACTGTCCGATGTCGTTGTCCAGGGATCAAACAACCAATGCAAATGCAAATGCAAATTATCAAAATAACCCAATTACCAAATGCACTCCACTTCCAAATGCTACCAAATGCAAATGCAAATTACCAAATTACGCTGTGGAATGATCCAATTACCACTTCCAAATGCTTCCAATGCTTCAAAATTACCAAATTACCACTTGGCTGCAATGCTTCCAATTACCACTTGTGTGCACTTTTATACCAATTACCACTTGTGTGCACACTTTTATACAAATTACCAATTGTTCTCAAAATTACCAATTGTTCTCAAATTTATCAACGATTGGCTTCAAACTTGGTTGAAAATTACAAAGATTGATT	1426 TCTCAAACTACCACGACCTCCCACGAGCATTCAGGGTCCTGACCACCACC 1485 11426 TCTCCAAACTACCACGACCTCCCACGAGCATTCAGGGTCCTGACCACCACC 1485 11805 TCTCGAAACCACACACGTAGGACGACACCACCACGTCCTACCACCTCCACCACCACCACGTCCTACACGTCCTACCACCACCACCACGTCCTACACGTCCTACACGTCCTACACGTCCTACACGTCTACACGTCTCCACGAGACACTACACGAGACACTACACACGTACACACAC	1666 GCCATTCTGGTGACAGTGTATATGTATCACCATCCAACATCAGCAGCATCTTCTTC 1725
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TICCATGGTTCACAAGGAACATCTCCGGTGGACTTGCCAGGAGTGTGACGAGA 2139
                               AACTCAGACTTGTACAAGACACCATGTACAATGATTAAAGAATTCCCTAGTG 2079
ATTTAAGACAAACAGACACACAACCCACAACCACACAAAGGAGCCCTAAA 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ovides novel human stem cell growth factor-like polynucleotides encoding them. The polypeptides having factor-like activity, can be expressed by standard odology. The polynucleotides and polypeptides can be ifferentiation of embryonic and adult stem cells to give t cell types. They may also be used in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor-like polypeptide; leukemia; hemophilia; human; ease; Alzheimer's disease; nutritional supplement; ropic; neuroprotective; hemostatic; antisense-therapy; ll proliferation; stem cell growth factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mize NK, Childs J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor-like polypeptide encoding cDNA.
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123..1712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; cDNA; 3095 BP.
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000S-0545714.
000S-0547358.
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leukemia, hemophilia, and degenerative diseases like Alzheimer's disease. They may also be utilized to generate new tissues and organs that may ald patients in need of transplants. They can also be used as nutritional supplements. The present sequence represents a stem cell growth factor-like polypeptide encoding cDNA. 88888888

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> T; 0 other; 804 ŝ 654 687 C; 3095 BP; 950 A; Seguence

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Query Best L Matche	Match Local S es 1700	65.2%; Score 1440.4; DB 22; Length 3095; imilarity 84.3%; Pred. No. 0; ; Conservative 0; Mismatches 291; Indels 25; Gaps 6;
٥y	168	3CCCCATCCCCAGGGATAACCCCGGAGCCCAGGGTCTCAAGAAAAATTCGTT
QQ	35	GTTTGGCCCGGTCGTGCCTATTGCATCGGGAGCCCCC
Oy Dp	228	GGCAGGGAGAGAGGTCGCGGCAGCGGCATGGCAAGGTTCCGGAGGGCCGACCTGGCCGC 287 
٥٧	288	SGAGITATGITACITIGICACITITIAACAGACCGGITCCAGITCGC
qq	155	
Qy	348	GACACCATACCAATGATTGGATTTATGAAGTTACAAACGCTTTTCCTT
qq	215	GAGACCAAATCCTTGATTGGCAGTATGGAGTTACTCAGGCCTTCCCTC
QY	408	AGAGGGGGTAGAAGTGGACTCTCAAGCATACAACCACAGGTGGAAAAGAAATGTGGACCC 467
QQ	275	AGGAGGTGGAAGTTGATTCACACGCGTACAGCCACAGGTGGAAAAGAAACTTG
0y	468	TITIAAGGCAGTAGACACAACAGAGCCAGCATGGGCCAAGCCTCTCCAGAGGG 527
QQ	335	CANGGCGGTAGACACGAACCGAGCGTCGGCCAAGACTTCTCTGAGCCCAAAA
οy	528	GTTCACTGACTGCTACTGGATGACGGACAATAACACCCCAGATAGAGGAGACAC 587
QQ	395	CTTCACAGACCTGCTGCTGGTGGTGTGTGTGTGTGTGTGT
ΟŸ	588	GGATCACAATTACTACATTTCTCGGATATATGGTCCAGCGGATTCTGCCAGCGGGATCT 647
ବୁ	455	AGACCACAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTT 514
٥y	648	IAACATAGACCAATGGAAAAAGACAAAGTGAAGATTCACGGGATACTT
οp	515	GGGTGAACATAGACCAAAAGATAAAGTGAAGATTCATGGAATATT
0 <i>y</i>	708	CACTCATCGGCAAGCTGCAAGAGAGATCTGTCCTTCGATTTTCCATTTTATGGTCATTT 767
Dβ	575	
ΟŊ	768	TCTAAATGAAGTCACTGTGGCAACTGGGGGTTTCATATATACTGGAGAAGTTGTACATCG 827
Ωp	635	TACGIGAAATCACIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGI
φ.	828	AATGCICACAGCTACACAGTATATAGCTCCTTTAATGGCAAATTTTGATCCCAGTGTATC 887
ΩD	695	SCIAACAGCCACACACATACATAGCACCTTAATGGCAAATTTCGATCCCAGT
Qy	888	CAGAAATTCAACTGTCAGATATTTTGATAATGGCACAGCTCTTGTTGTCCAGTGGGACCA 947
qq	755	CCAGTGG
Qy	948	ACTCCTCA
QΩ	815	GIACATCTCCAGGATAATTATAACCTGGGAAGCTTCACATTCCAGGCAACCTTC
QY	1008	GGACGGGCCCATCATCGATACAAAAAACCCCTGTCGTCACACACA
Db	875	AAGTT
QY	1068	TACCAACCATCCAGTGAAAGTCGGGTTGTCTGATGCATTTGTCGTGGTCCACAGGATCCA 1127

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1484 1664 1724 1784 1844 935 AACCAATCCATCCAGTGAAAGTCGGACTGTCCGATGCATTTGTCGTTGTCCTTGTCCCA CCCGGAAGAGGTACAGTCAAAAGAGAAGATGTGTGAGAAGAACAAGCCAGGAGAGA---C 1545 AGCCCTACATCTCAAAGACAGTGGAGCCTCCACAGATGACAGTGCAGCTGAGAAGAAAGG 1605 AGGAACCCTCCATGCAGGCCTCATTGTTGGAATTCTCATCTTGGTCCTCATTATAGCAGC 1589 TATTGAGAGACGCCCAAGCAGATGGCCTGCGATGAAGTTTAGAAGAGGCTCTGGACATCC TGCTTATGCATTTAAGACAAACAGACACACACCACAAGCCACAAAGGAGCCCTAA 1964 ACTGCTGTAGACAGAAGGGCGACGAGTTTCTGGACAAGCCCCAGGC----AACAT TGAAAGGAAAACTCAGACTTGTACAAGACACCATGTACAATGATTAAAAGAATTCCCTAGT GGAATGTCATCTATAGTTCACTCGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAG CAATGGTTGTGGCCCTTGTGTCTCCTCGCAGATTGGTTTCAACTGCAGTTGGTGCAGCAA ACTICAAAGAIGCICCAGIGGAITIGAICGCCAICGGCAGGACIGGGIGGACAGIGGAIG 1235 CCCTGAAG-----AGTCAAAAGAGAAGATGTGTGAGAATACAGAACCAGTGGAAACTTC 1425 ATCTCAAACTACCACGACCTCCCACACGACCATGCAATTCAGGGTCCTGACCACCAC TGCCTATGCAGAAGTTGAACCAGTTGGAGAAAGAAGGTTTTATTGTATCAGAGCAGTG GGAATGACATCCATGGTTCACAAGGAACATCTCCGGTGGACTTGCCAGGAGTGTGACGAG ATGACGATGCTTTTGGTTTAGGTGCAGGGTTGCAAA 2174 1055 1308 1368 1904 1188 1248 1785 2019 1879 

BP

GATTGGCAGTATGGAGTTACTCAGGCCTTCCCTCACAGAGGAGGAGGTGGAAGTTGAT

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Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulat; antianglogento; tumour; neoanglogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth -
                                                                                                                                                                                                                                                                                    Human Tumour Endothelial Marker polynucleotide SEQ ID NO 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 129-130; 331pp; English.
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                                                                     ABL92080 standard; cDNA; 2157
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11-AUG-2000; 2000US-224360P.
11-APR-2001; 2001US-282850P.
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                                                                                                                                                                                                                 (first entry)
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                                                                                                                                           ABL92080;
RESULT 6
ABL92080
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a Lumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antianglogenic activity. They are useful for inhibiting tumour growth, necanglogenesis in gubjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90702-ABB90789) are disclosed, as are marker oilgounclectided sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92191: normal endothelial markers (NEM) ABL91995.

Sequence 2157 BP; 694 A; 490 C; 463 G; 510 T; 0 other;

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                                                                                          TGTCACTTTTTAACAGACCGGTTCCAGTTCGCCCACGGGGAGCCTGGACACCATACCAAT 366
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                                             GATTGGATTTATGAAGTTACAAACGCTTTCCTTGGAATGAAGAGGGGGTAGAAGTGGAC
                                                                                                          25; Gaps
Query Match 65.4%; Score 1423.8; DB 24; Length 2157; Best Local Similarity 85.7%; Pred. No. 0; Marches 1660; Conservative 0; Mismatches 252; Indels 25;
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          AACAGAGCCAGCATGGGCCAAGCCTCTCCAGAGTCCAAAGGGTTCACTGACCTGCTACTG
                                                                     GATGACGGACAGGACAATAACACCCAGATAGAGGAGGACACGGATCACAATTACTACATT
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                                                                                                                                            667 AIGGAAAAGACAAAGIGAAGAITCACGGGAIACITICCAACACICAICGGCAAGCIGCA
                                                                                                                                                                                            481 AGAGTGAATCTGTCCTTCGATTTTCCATTTTATGGCCACTTCCTACGTGAAATCACTGTG
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TCTCAAGCATACAACCACAGGTGGAAAAGAAATGTGGACCCTTTTAAGGCAGTAGACACA
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2000US-222599P. 2000US-224360P. 2001US-282850P.

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normal endothelial marker; pan-endothelial marker; immunostimulant;
antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
psoriasis; gene; ss.
                                         AGAIGGCCACCAATGAAGTTTCGAAGAGGCTCAGGACACCCTGCCTATGCAGAAGTTGAA
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07-FEB-2002

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                                                                                                                                                                                                                                                          The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) Protein selected from ABB90732, ABB90740, ABB90744, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antianglogenic activity. They are useful for inhibiting tumour growth, necentycogenic activity. They are useful for inhibiting tumour growth, necentycogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, and tabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse ABB90721.ABB90789 are disclosed, as are marker oligonucleotide asquences: tumour endothelial markers (TEM) ABB19906.ABB192041 and ABB192143-ABB192191; normal endothelial markers (NEM) ABB191995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 IGTCACTITITAACAGACCGGTTCCAGTTCGCCCACGGGGGGGCCTGGACACCATACCAAT 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.4%; Score 1423.8; DB 24; Length Best Local Similarity 85.7%; Pred. No. 0; Matches 1660; Conservative 0; Mismatches 252; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2159 BP; 696 A; 490 C; 463 G; 510 T; 0 other;
                                                                                                                                                                                                            Disclosure; Page 153-154; 331pp; English.
WPI; 2002-291856/33.
P-PSDB; ABB90734.
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Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183; PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308; PRO1108; PRO1272; PRO4419; PRO4999; PRO7170; PRO448; PRO353; PRO1316; PRO1600; PRO5940; PRO533; PRO317; PRO187; PRO1411; PRO4356; PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO2600; PRO2630; PRO50096; PRO6009; PRO6009; PRO6009; PRO50096; PRO50096; PRO60096; PRO
ACAAGGAACATCTCCGGTGGACTTGCCAGGAGTGTGACGAGATGACGATGCTTTTGGTTT
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99WO-US21040.
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17-AUG-1999;
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The present sequence encodes a human secreted and transmembrane polypeptide. The specification describes human polypeptides, designated PRO196, PRO196, PRO198, PRO199, PRO1994, PRO1994, PRO1996, PRO1996, PRO1996, PRO609, PRO5050, PRO286, PRO246, PRO246, PRO246, PRO246, PRO246, PRO246, PRO1996, PRO1996, PRO6003, PRO5050, PRO250, PRO250, PRO250, PRO250, PRO250, PRO250, PRO250, PRO1996, PRO1096, PRO6003, PRO5060, PRO5
                                                                                                                                                                                                                                               Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
Ferrara M, Rong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Goddowski PJ, Gurney AL, Allyavin LJ, Mather JP, Napier MA, Pan J;
Paoni NF, Roy MA, Stewart TR, Tunas D, Watanabe CK, Williams PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule encoding
transmembrane polypeptide is useful for
of related polypeptides
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20-MAR-2000; 2000WO-US07377;
30-MAR-2000; 2000WO-US08439.
15-MAY-2000; 2000WO-US13358.
17-MAY-2000; 2000WO-US13705.
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                                                                                                                                                                             (GETH ) GENENTECH INC.
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P-PSDB; AAB31211.
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Wood WI, Zhang Z;
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a PRO polypeptide which is a gene therapy and identification

Sequence 2557 BP; 718 A; 639 C; 615 G; 585 T; 0 other;

é 637 412 472 GAGTTATGTTACTTTGTCACTTTTTAACAGACCGGTTCCAGTTCGCCCACGGGGAGCCTG 352 697 757 877 997 233 GGGAGAGATCGCGGCAGCGCATGGCAAGGTTCCGGAGGCCGACCTGGCCGCAGCAG GACACCATACCAATGATTGGATTTATGAAGTTACAAACGCTTTTCCTTGGAATGAAGAGG AGGCAGTAGACACAAACAGAGCCAGCATGGGCCAAGCCTCTCCAGAGTCCAAAGGGTTCA CTGACCTGCTACTGGATGACGGACAGGACAATAACACCCAGATAGAGGAGGACACGGATC ACAATTACTACATTTCTCGGATATATGGTCCAGCGGATTCTGCCAGCCGGGATCTGTGGG CAGACCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGATACAGACC Gaps 2557; 25; DB 22; Length Score 1423.4; DB 22; Lengt Pred. No. 0; 0; Mismatches 264; Indels Query Match 65.4%; Best Local Similarity 85.2%; Matches 1662; Conservative ( 578 293 638 353 413 473 818 878 533 9 % g 97 97 97 97 64 B 64 ò g à g

1298 ATCTCCAGGATAATATATAAACTGGGAAGCTTCACATTCCAGGCAACCCTGCTCATGGATG GGCGCATCATCTTTGGATACAAAGAAATCCCTGTCTTGGTCACACAGATAAGTTCTACCA 1073 ACCATCCAGTGAAAGTCGGGTTGTCTGATGCATTTGTCGTGGTCCACAGGATCCAGCAAA TACCCAATGTTCGAAGAAGAACAATTTATGAATATCACCGAGTAGAACTACAAATGTCCA AAATTACCAACATCTCAGCTGTGGGAGATGACTCCACTTCCCACATGTCTCCAGTTCAATG GITGIGGCCCTIGIGICCTCGCAGALIGGILTCAACTGCAGITGGTGCAGCAACITC 1430 AAACTACCACGACCTCCCACACGACCATGCAATTCAGGGTCCTGACCACCACCAGGA TACATCTCAAAGACAGTGGAGCCTCCACAGATGACAGTGCAGCTGAGAAGAAAGGAGGAA AGAGACGCCCAAGCAGATGGCCAGCAATGAAGTTTCGAAGAGGCTCAGGACACCCTGCCT ATCGGCAAGCTGCAAGAGTGAATCTGTCCTTCGATTTTTCCATTTTATGGTCATTTTCTAA ATGAAGTCACTGTGGCAACTGGGGGTTTCATATATACTGGAGAAGTTGTACATCGAATGC TCACAGCTACACAGTATATAGCTCCTTTAATGGCAAATTTTGATCCCAGTGTATCCAGAA 893 ATTCAACTGTCAGATATTTTGATAATGGCACAGCTCTTGTTGTCCAGTGGGACCATGTCC ACCTGCAGGATAATTACAACCTGGGAAGCTTCACATTCCAGGCCACACTCCTCATGGACG AAAGATGCTCCAGTGGATTTGATCGCCATCGGCAGGACTGGGTGGACAGTGGATGCCCGG AAGAGGTACAGACAAAAGAGAAGATGTGTGAGAAGACAGAGCCAGGAGAGA----CATCTC GAGCTGTGACATCTCAGATGCCTACCAGCCTGCCTACAGAAGATGACACGAAGATAGCCC CCCTCCATGCAGGCCTCATTGTTGGAATTCTCATCTTGGTCCTCATTATAGCAGCGGCCA **TTAACATAGACCAAATGGAAAAAGACAAAGTGAAGATTCACGGGATACTTTCCAACACTC** 1013 1133 1193 1598 1373 1718 1772 773 1118 833 1178 1253 1313 1490 1832 1550 1610 1670 713 953 셤 ò 셤 à 셤 ò 셤 δ 셤 δ 셤 δ ద δy 셤 Qγ 원 οy d ă g ŏ a ă g ò 셤 Š g ò 염 ò à à

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2024 GGAAAACTCAGACTTGTACAAGACACCATGTACAATGATTAAAGAATTCCCTAGTGGAAT
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treatment of leukemia, hemophilia, and degenerative diseases like
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07-APR-2000; 2000US-0545714.
11-APR-2000; 2000US-0547358.
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                                                 The invention provides novel human stem cell growth factor-like polypeptides and polynucleotides encoding them. The polypeptides having stem cell growth factor-like activity, can be expressed by standard recombinant methodology. The polynucleotides and polypeptides can be used to induce differentiation of embryonic and adult stem cells to give used to induce different cell types. They may also be used in the treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease. They may also be utilized to generate new tissues and organs that may aid patients in need of transplants. They can also be used as nutritional supplements. The presents a stem cell growth factor-like polypeptide coding sequence.
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86.9%; Pred. No. 0;
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tissues
Alzheimer's disease and to generate new
                             Claim 1; Page 140-141; 154pp; English.
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Matches 1387; Conservative
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                                                                                                       ATTTATGAATATCACCGAGTAGAACTACAAATGTCCAAAATTACCAACATCTCAGCTGTG 1215
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM4213) with nootropic. The encoded polypeptides (AAM3642-AAM4213) with nootropic. Immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous asystem claimer's, parkinson's disease, mayotrophic lateral sclerosis, and shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, caltivity, chemotractic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c.Ns alsonders.

Note: The sequence data for this patent did not form part of the printed specification.
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Zhang J;
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Yang Y,
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Wang J, Wang Z, Wehrman T, Xu C, Xue AJ,
Zhao QA, Zhou P, Goodrich R, Drmanac RT;
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25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
19-CCT-2000; 2000US-0653450.
29-NOV-2000; 2000US-053344.
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P-PSDB; AAM40853.
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09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
19-OCT-2000; 2000US-0653450.
29-NOV-2000; 2000US-073744.
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P-PSDB; AAM40854.
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and
                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzhehmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J;
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Yang Y,
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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specification

T; 0 other; Sequence 2668 BP; 721 A; 517 C; 579 G; 851

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Score 1195.2;
Pred. No. 0;
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 Query Match 54.9%;
Best Local Similarity 87.0%;
Matches 1390; Conservative
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AAACTGCTGTAGACAGAAGGGGGACGAGATTTCTGGACAAGCCCAGG----AAC 2016
                                                                                                                                                                                               /transl_except= (pos:859..862,aa:Phe)
/note= "This codon has an apparent 1 nucleotide insertion
                                                                                                                                                                                                                                                                                   2017 ATTGAAAGGAAAACTCAGACTTGTACAAGACACCATGTACAATGATTAAAGAATTCCCTA
                                                                                 1509 TITATIGAGAGACGCCCAAGCAGAIGGCCIGCGAIGAAGTITAGAAGAGCICTGGAAT
                                                                                                                                                                     CCTGCCTATGCAGAAGTTGAACCAGTTGGAGAAAGAAGGATTTTATTGTATCAGAGCAG
                                                                                                                                                                            TITGCITALGCALTITAAGACAAACAGACACACAAACCCACACACACAAAGGAGCCCI
                                                                                                                                                                                                                                   GTGGAATGACATCCATGGTTCACAAGGAACATCTCCGGTGGACTTGCCAGGAGTGTGACG
                                                                                                                                                                                                                                                                                                                        ATAGCCCTACATCTCAAAGACAGTGGAGCCTCCACAGATGACAGTGCAGCTGAGAAGAAA
                                                                                                                                          TTCATTGAGAGGCCCAAGCAGATGGCCAGCAATGAAGTTTCGAAGAGGCTCAGGACAC
                                                                                                                                                                                                                                                                                                                                                   AGATGACGATGCTTTTGGTTTAGGTGCAGGGTTGCAAA 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense-therapy; gene-therapy; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                       NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide 784_3137 contig SEQ ID
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The invention relates to an isolated human polynucleotide (AAH75398) encoding a novel polypeptide (AAG64527) useful in antisense-therapy and gene-therapy, in diagnostics, forensics, gene mapping and identification of mutations responsible for genetic disorders and other traits. Polynucleotide sequences with potential homology were also identified (AAH93283-AAH93356).
                                                         nucleotide deletion
                                                                                                                                                                                                                                                                                                                                                                                    diseases, diagnostics, raising
which alters the reading frame"
/transl_except= {pos:879..884,aa:Pro}
/transl_except= {pos:979..914,aa:Ser}
/transl_except= {pos:927..928.aa:Ser}
/rote= "This codon has an apparent 1 nucle
which alters the reading frame"
/product= "human protein SEQ ID NO 2"
/partial
/note= "CDS lacks an initiation codon"
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                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide for treatment antibodies and research use -
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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P-PSDB; AAG64527.
                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
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CAIGTCCACCIGCAGGATAATTACAACCIGGGAAGCTICACATTCCAGGCCACACTCCTC 1005
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                                                                                                                                 TCCAGAAATTCAACTGTCAGATATTTTGATAATGGCACAGCTCTTGTTGTCCAGTGGGAC
                                           586 ACGGATCACAATTACTACATTTCTCGGATATATGGTCCAGCGGATTCTGCCAGCCGGGAT
                                                                                                                                                               CGAATGCTCACAGCTACACAGTATATAGCTCCTTTAATGGCAAATTTGATCCCAGTGTA
                            25; Gaps
            Score 1195.2; DB 22; Length 2668; Pred. No. 0; 0; Mismatches 183; Indels 25;
Sequence 2668 BP; 851 A; 579 C; 517 G; 721 T; 0 other;
             Query Match 54.9%;
Best Local Similarity 87.0%;
Matches 1390; Conservative
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1365 1482 1843 TGCTAAAATT-TAGGACAGAGCACCAGTACTGGCTTACAGGTGTTAAGACTAAAAC 1901 GIGGAAIGACAICCAIGGIICACAAGGAACAICICCGGIGGACIIGCCAGGAGIGIGACG 2136 919 TGCCCGGAAGAGGTACAGTCAAAAGAGAAGATGTGTGAGAAGACAGAGCCAGGAGAGACAAA TGCCCTGAAG-----AGTCAAAAGAGAAGATGTGTGAGAATATGAGAACAGAAGAAAACT AAACTTCAAAGATGCTCCAGTGGATTTGATCGCCATCGGCAGGACTGGGTGGACAGTGGA 860 TCTTCTCGAACCACCACAACATAGGAGCGACAACCACCAGTTCAGGGTCCTAACTACC ATAGCCCTACATCTCAAAGACAGTGGAGCCTCCACAGATGACAGTGCAGCTGAGAAGAAA GCGGCCATTCTGGTGACAGTGTATATGTATCACCATCCAACATCAGCAGCAGCATCTTC 1100 ACAGCCATTCTTGTGACAGTCTATATGTATCACCACCAACATCAGCAGCAGCATCTTC 1723 TICATTGAGAGGCCCCAAGCAGAATGGCCAGCAATGAAGTTTCGAAGAGGCTCAGGACAC CAGCAAATACCCAATGTTCGAAGAAGAACAATTTATGAATATCACCGAGTAGAACTACAA TTCAATGGTTGTGGCCCCTTGTGTGTCTCGCAGATTGGTTTCAACTGCAGTTGGTGCAGC ---TCTCAAACTACCACGACCTCCCACACGACCACCATGCAATTCAGGGTCCTGACCACC **ATGGACGGCCCATCATCTTTGGATACAAAGAAATCCCTGTCTTGGTCACACAGATAAGT** TCTACCAACCATCCAGTGAAAGTCGGGTTGTCTGATGCATTTGTCGTGGTCCACAGGATC 1366 920 1543 1902 1186 626 989 1306 806 1426 1483 1663 9001 1126 1246 266 g g 2 Q b Q ŏ g g 9 δ g ò g δ 셤 ď 셤 9 2 2 δ o o o à 셤 ŏ à 엄 ò 윱 ò d ōλ g 5 Q ò

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ACAGACCACAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGAT
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The invention provides novel human stem cell growth factor-like polypeptides and polynucleotides encoding them. The polypeptides having stem cell growth factor-like activity, can be expressed by stendard recombinant methodology. The polynucleotides and polypeptides can be used to induce differentiation of embryonic and adult stem cells to give rise to different cell types. They may also be used in the treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease. They may also be utilized to generate new tissues and organs that may aid supplements. The present sequence represents a stem cell growth factor-like polypeptide encoding cDNA.
                                                                                                                                                                                          Stem cell growth factor-like polypeptide; leukemia; hemophilia; human; degenerative disease; Alzhelmer's disease; nutritional supplement; cytostatic; nootropic; neuroprotective; hemostatic; antisense-therapy; gene-therapy; cell proliferation; stem cell growth factor; ss.
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                               AGATGACGATGCTTTTGGTTTAGGTGCAGGGTTGCAAA 2174
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107..1285
/*tag= a
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07-APR-2000; 2000US-0545714.
11-APR-2000; 2000US-0547358.
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P-PSDB; AAB85392.
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Chao C;
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1005 1185 1305 1365 1425 1482 1542 1602 GGAGGAACCCTCCATGCAGGCCTCATTGTTGGAATTCTCATCTTGGTCCTCATTATAGCA 1662 1159 625 685 859 885 145 825 CGAATGCTCACACCACTACACAGTATATAGCTCCTTTAATGGCAAATTTTGATCCCAGTGTA CATGTCCACCTGCAGGATAATTACAACCTGGGAAGCTTCAACATTCCAGGCCACACCTCCTC 1186 ATGTCCAAAATTACCAACATCTCAGCTGTGGAGATGACTCCACTTCCCACATGTCTCCAG 1306 AAACTTCAAAGATGCTCCAGTGGATTTGATCGCCATCGGCAGGACTGGGTGGACAGTGGA TGCCCGGAAGAGGTACAGTCAAAAGAGAAGATGTGTGAGAAGACAGAGACCAGGAGAGACA ---TCTCAAACTACCACGACCTCCCACACGACCACCATGCAATTCAGGGTCCTGACCACC 860 TCTTCTCGAACCACCACAAACATAAGAAGGAACAACCAAGTTCAGGGTCCTAACTACC 1543 ATAGCCCTACATCTCAAAGACAGTGGAGCCTCCACAGATGACAGTGCAGCTGAGAAAAA 1100 ACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACATCAGCAGCAGCAGCATCTTC TTTCTAAATGAAGTCACTGTGGCAACTGGGGGTTTCATATATACTGGAGAAGTTGTACAT ATGGACGGCGCATCATCTTTGGATACAAAGAAATCCCTGTCTTGGTCACACAGATAAGT 506 TCAACCAATCATCAGTGAAAGTCGGACTGTCCGATGCATTTGTCGTTGTCCACAGGATC CAGCAAATACCCAATGTTCGAAGAACAATTTTATGAATATCACCGAGTAGAACTACAA CTGTGGGTTAACATAGACCAAATGGAAAAAGACAAAGTGAAGATTCACGGGATACTTTCC 1040 셤

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                                                                                                                                                                                           GTGGAATGACATCCATGGTTCACAAGGAACATCTCCGGTGGACTTGCCAGGAGTGTGACG 2136
                                                                                                                                                                                                 Stem cell growth factor-like polypeptide; leukemia; hemophilia; human; degenerative disease; Alzheimer's disease; nutritional supplement; cytostatic; nootropic; neuroprotective; hemostatic; antisense-therapy; gene-therapy; cell proliferation; stem cell growth factor; ss.
                                             TGCTAAAATTT-TAGGACAGAGCAGCACCAGTACTGGCTTACAGGTGTTAAGACTAAAAC
                                                                                                1902 ITTGCTTATGCATTTAAGACAAACAGACACACACACCACACACCACAAAGGAGCCCT
                                                                                                                               AAACTGCTGTAGACAGAAGGGCGACGAGATTTCTGGACAAGCCCAGCCCAGG-----AAC
                                     CCTGCCTATGCAGAAGTTGAACCAGTTGGAGAGAAAGAAGGTTTTATTGTATCAGAGCAG
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07-APR-2000; 2000US-0545714.
11-APR-2000; 2000US-0547358.
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P-PSDB; AAB85393.
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1066 TCTACCAACCATCCAGTGAAAGTCGGGTTGTCTGATGCATTTGTCGTGGTCCACAGGATC 1125
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                                                                                                                                                                       The invention provides novel human stem cell growth factor-like polypeptides and polymoclectides encoding them. The polypeptides having stem cell growth factor-like activity, can be expressed by standard recombinant methodology. The polymoclectides and polypeptides can be used to induce differentiation of embryonic and adult stem cells to give rise to different cell types. They may also be used in the treatment of leukenia, hemophilia, and degenerative diseases like Alzheimer's disease. They may also be utilized to generate new tissues and organs that may also patients in need of transplants. They can also be used as nutritional supplements. The present sequence represents a stem cell growth factor-like polypeptide encoding cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 AATACTCATCGGCAAGCTGCAAGAGTGAATCTGTCCTTCGATTTTCCATTTTATGGCCAC
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Isolated polypeptide with stem cell growth factor-like activity for treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease and to generate new tissues and organs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 2668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2668 BP; 851 A; 579 C; 517 G; 721 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.9%; Score 1195.2;
87.0%; Pred. No. 0;
11ve 0; Mismatches
                                                                                                                  Claim 1; Page 129-131; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.0
Matches 1390; Conservative
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1783 CCTGCCTATGCAGAAGTTGAACCAGTTGGAGAAAGAAGGTTTTATTGTATCAGAGCAG 1842
                                                                                                                                                                                                                                                                                                                                     1962 AAACTGCTGTAGACAGAAGGGCGACGAGATTTCTGGACAAGCCCAGCCCAGG----AAC 2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2017 ATTGAAAGGAAAACTCAGACTTGTACAAGACACCATGTACAATGATTAAAGAATTCCCTA 2076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2077 GIGGAAIGACAICCAIGGIICACAAGGAACAICICCGGIGGACIIGCCAGGAGIGIGACG 2136
                                                                                                               1543 ATAGCCCTACATCTCAAAGACAGTGGAGCCTCCACAGAGACAGTGCAGCTGAGAAGAAA 1602
                                                                                                                                                                     980 ATAGCACTACATCTAAAAGATAATGGAGCTTCTACAGATGACAGGTGCAGCTGAGAAA 1039
                                                                                                                                                                                               1603 GGAGGAACCCTCCATGCAGGCCTCATTGTTGGAATTCTCATCTTGGTCCTCATTATAGCA 1662
                                                                                                                                                                                                           TTCATTGAGAGGCCCCAAGCAGATGGCCAGCAATGAAGTTTCGAAGAGGCTCAGGACAC 1782
                                                                                                                                                                                                                                                                                                                                                                  1843 TGCTAAAATTT-TAGGACAGAGCAGCACCAGTACTGGCTTACAGGTGTTAAGACTAAAAC 1901
                                                                                                                                                                                                                                                                                                                                                                                                          ---TCTCAAACTACCACGACCTCCCACACGACCACCATGCAATTCAGGGTCCTGACCACC 1482
                                          920 ACCAGAAGAGGAGTGACTTCTCAGTTTCCCACCAGCCTCCCTACAGAAGATGATACCAAG
                                1366 TGCCCGGAAGAGGTACAGTCAAAAGAGAAGATGTGTGAGAAAGACAGAGCCAGGAGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATGACGATGCTTTTGGTTTAGGTGCAGGGTTGCAAA 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATTATAATGCTTTGGCTTAGGTGCAGGGTTGCAAA 1607
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GIGICGCCCCAICCCCAGGGAIAACCCCGGAGCCCAGGGTCTCAAGAAAAAIICGIIGG 228
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                                                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
                                                                                                                                                              Human polynucleotide SEQ ID NO 426.
                                                AAI58223 standard; cDNA; 2275
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(first entry)

22-OCT-2001

RESULT 15
AA15823
ID AA15823
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AC AA158
DT 22-OC'
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DE HUMAN
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HUMAN
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HUMAN
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KW HUMAN

AAI58223;

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, fimunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system, such as peripheral nervous system, auch as peripheral nervous system, and a seases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral science, and suppression, utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, hammostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ITGTGTCTCAGTTGGGGGCTGCGAGGGTGACAAGTTGCAGTGAGAGCTCCCGAAGTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 AGAGGGTTCAGCT------GTCTCTCCTTCACTTCTGTTACCCGGAGTGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTAGCGAAACTGTCAGAGGCCTCCGGATCCCACCCAAGACTCACCAGCAGAGCTCGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 2275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
53.5%; Score 1165.2; DB 22; Length
Best Local Similarity 82.3%; Pred. No. 0;
Matches 1410; Conservative 0; Mismatches 273; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2275 BP; 571 A; 596 C; 579 G; 529 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 426; 10078pp; English.
                                                                                                                                                                                                                       21-JAN-2000; 2000US-0488725.
25-ARR-2000; 2000US-0552317.
09-UUL-2000; 2000US-0598042.
19-UUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-062191.
19-CCT-2000; 2000US-063336.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                       26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-442253/47.
P-PSDB; AAM39067.
                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification.
                                                                                                               WO200153312-A1
                                           leukaemia; ss
                                                                               Homo sapiens.
                                                                                                                                                   26-JUL-2001
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Wang J, Y
Zhao QA,
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800	348 862	408	468 982	528	588 1102	648	708	768 1282	828	1402	948 1462	1008	1068	1128	1188	1248	1308
29 GCAGGGGAGAGGCTCGCGGCAGCGCCATGGCAAGGTTCCGGAGGCCCGACCTGGCCGCAACTTCTGAGGAGGTGCGACCTGGCCGCAAGGTTCCCGAAGGCGACCTGGCCGCTGCCGCTAAGGAGGCGACCTGGCCGCTTAAGGAGGCGACCTGGCCGCTTAAGGAGGCGACCTGGCCGCTTAAGGAGCGACCTGGCCGCTTAAGGAGCGACCTGGCCGCTTAAGGAGCGACCTGGCCGCTAAGGCGAGCGGACCTGGCCGCTAAGAGAGCGAACTGGCCGCTAAGAGCGAACTGGCCGCTAAGAGAGCGAACTGGCCGCTAAGAGAGCGAACTGGCCGCTAAGAGAGCGAACTGGCCGCTAAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	289 GCAGGAGTIATGTIACTITTGTCACTTTTTAACAGACCGGTTCCAGTTGCCCCACGGGGAG 	349 CCTGGACACCATACCAATGATTGATTTATGAAGTTACAAAACGCTTTTCCTTGGAATGAA. 	409 GAGGGGGTAGAAGTGGACTCTCAAGCATACAACCAGGTGGAAAAGAAATGTGGACCCT 	469 TTTAAGGCAGTAGACACAAACAGAGCCAGCATGGGCCAAGCCTCCCACAGTCCAAAGGG 	529 TTCACTGACCTGCTACTGGATGACGGACAGGACAATAACACCCAGATAGAGGAGACACG 	589 GATCACAATTACTACATTTCTCGGATATATGGTCCAGCGGATTCTGCCAGCCGGGATCTG	649 TGGGTTAACATAGACCAAATGGAAAAGACAAAGTGAAGATTCACGGGATACTTTCCAAC 	709 ACTCATCGGCAAGCTGCAAAGTGAATCTGTCCTTCGATTTTCCATTTATGGTCATTTT 	769 CTRARATGRAGTCACTGTGGCAACTGGGGGTTTCATATATACTGGAGAAGTTGTACATCGA 	829 AIGCICACACACACACAGTATAIAGCICCITIAAIGGCAAAITITGAICCCAGIGIAICC	889 AGAAAITCAACIGICAGAIAIIIIGAIAAIGGCACAGCICIIGIIGICCAGIGGGACCAI 	949 GICCACCIGCAGGAIAATTACAACCIGGGAAGCTICCACATTCCAGGCCACACTCCTCATG	009 GACGGGCGCATCATTGGATACAAGAAATCCCTGTCTTGGTCACACAGATAAGTTCT 	069 ACCAACCATCCAGTGAAAGTCGGGTTGTCTGATGCATTGTCGTGGTCCAGGGATCCAG 	129 CAAATACCCAATGTTCGAAGAAGAACAATTTATGAATATCACCGAGTAGAACTACAAATG 	189 TCCAAAATTACCAACATCTCAGCTGTGGACATGACTCCACTTCCCACATGTCTCCAGTTC	249 AAIGGITGIGGCCCIIGIGICCICGCAGAIIGGITTCAACIGCAGIIGGIGCAGCAAA 
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Search completed: June 23, 2003, 19:45:44 Job time : 494 secs